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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=5; day=27; hr=13; min=35; sec=56; ms=931;]

=====

Reviewer Comments:

SEQUENCE LISTING

<110> Nordheim et al.

<120> Method For Detecting Biomolecules

Please insert the following mandatory numeric identifiers and their responses below the <120> line:

<130> this represents the file reference number: the response is usually the attorney docket number

<140> US 10/527,055 (this is the current application number)

<141> 2005-05-18 (this is the current application filing date)

<210> 1

<211> 9

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 1

AVFPSIVGR

Several errors above: 1) the "<212> PROTEIN" line is invalid: per the Sequence Rules, use PRT to denote an amino acid sequence; 2) Please show "UNKNOWN" as "Unknown" (only the initial letter is in upper-case); 3) Please insert a mandatory "<220>" above the <223> line; <220> is mandatory whenever <221>, <222>, or <223> is shown. It is a "header" only: it never has a response; 4) although the <213> response is "Unknown", in the <223> response, please try to furnish more information regarding the source of the genetic material; also, you do not need to

indicate Figures; 5) do not use one-letter amino acids. Per the Sequence Rules, use three-letter amino acids, with one space between each amino acid. Please number the amino acids under every 5 amino acids, starting with "1"; do not use TAB codes between amino acid numbers: TABs cause misaligned numbers when processed: use space characters, instead. Please show a maximum number of 16 amino acids per line.

<210> 10

<211> 13

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 4 - Enolase 1, alpha non neuron

<400> 10

YITPDQLADLYK

Besides all of the errors listed in the first paragraph above, there is a discrepancy in this sequence: although the <211> response is "13", only 12 amino acids are shown. Please ensure, in subsequent sequences, that the <211> response matches the actual number of amino acids in the sequence.

Application No: 10527055 Version No: 1.0

Input Set:**Output Set:**

Started: 2010-05-27 10:29:07.908
Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
Total Warnings: 1923
Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

Error code	Error Description
E 310	Invalid sequence type in <212> in SEQID: (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (1)
W 112	Upper case found in data; Found at position(0) SEQID(1)
W 112	Upper case found in data; Found at position(1) SEQID(1)
W 112	Upper case found in data; Found at position(2) SEQID(1)
W 112	Upper case found in data; Found at position(3) SEQID(1)
W 112	Upper case found in data; Found at position(4) SEQID(1)
W 112	Upper case found in data; Found at position(5) SEQID(1)
W 112	Upper case found in data; Found at position(6) SEQID(1)
W 112	Upper case found in data; Found at position(7) SEQID(1)
W 112	Upper case found in data; Found at position(8) SEQID(1)
E 310	Invalid sequence type in <212> in SEQID: (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
W 112	Upper case found in data; Found at position(0) SEQID(2)
W 112	Upper case found in data; Found at position(1) SEQID(2)
W 112	Upper case found in data; Found at position(2) SEQID(2)
W 112	Upper case found in data; Found at position(3) SEQID(2)

Input Set:

Output Set:

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Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
Total Warnings: 1923
Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

Error code	Error Description
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W 112	Upper case found in data; Found at position(5) SEQID(2)
W 112	Upper case found in data; Found at position(6) SEQID(2)
W 112	Upper case found in data; Found at position(7) SEQID(2)
W 112	Upper case found in data; Found at position(8) SEQID(2)
W 112	Upper case found in data; Found at position(9) SEQID(2)
E 310	Invalid sequence type in <212> in SEQID: (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
W 112	Upper case found in data; Found at position(0) SEQID(3) This error has occurred more than 20 times, will not be displayed
E 310	Invalid sequence type in <212> in SEQID: (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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Input Set:

Output Set:

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Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
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Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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Input Set:

Output Set:

Started: 2010-05-27 10:29:07.908
Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
Total Warnings: 1923
Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
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W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
E 310	Invalid sequence type in <212> in SEQID: (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
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E 310	Invalid sequence type in <212> in SEQID: (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
E 310	Invalid sequence type in <212> in SEQID: (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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Input Set:

Output Set:

Started: 2010-05-27 10:29:07.908
Finished: 2010-05-27 10:29:16.673
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 765 ms
Total Warnings: 1923
Total Errors: 306
No. of SeqIDs Defined: 153
Actual SeqID Count: 153

Error code	Error Description
E 310	Invalid sequence type in <212> in SEQID: (20) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Nordheim et al.

<120> Method For Detecting Biomolecules

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<210> 1

<211> 9

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 1

AVFPSIVGR

<210> 2

<211> 10

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 2

GYSFTTTAER

<210> 3

<211> 16

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 3

SYELPDGQVITIGNER

<210> 4

<211> 18

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 2 - Actin (isoform n.d.)

<400> 4

VAPEEHPVLLTEAPLNPK

<210> 5

<211> 13

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 3 - Heat shock protein cognate 70

<400> 5

DAGTIAGLNVLRD

<210> 6

<211> 18

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 3 - Heat shock protein cognate 70

<400> 6

TVTNAVVTVPAYFNDSQR

<210> 7

<211> 23

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 3 - Heat shock protein cognate 70

<400> 7

SINPDEAVAYGAAVQAAILSGDK

<210> 8

<211> 24

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 3 - Heat shock protein cognate 70

<400> 8

QTQTFTTYSNQPQGVLIQVYEGER

<210> 9

<211> 13

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 4 - Enolase 1, alpha non neuron

<400> 9

GNPTVEVDLYTAK

<210> 10

<211> 13

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 4 - Enolase 1, alpha non neuron

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YITPDQLADLYK

<210> 11

<211> 18

<212> PROTEIN

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<223> Fig. 4A - Spot 4 - Enolase 1, alpha non neuron

<400> 11

AAVPSGASTGIYEALRL

<210> 12

<211> 13

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 6 - Heat shock protein 110 kDa

<400> 12

VLATAFDTTLGGR

<210> 13

<211> 14

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 6 - Heat shock protein 110 kDa

<400> 13

AGGIETIANEYSDR

<210> 14

<211> 14

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 6 - Heat shock protein 110 kDa

<400> 14
 ELSTTLNADEAVTR

<210> 15
 <211> 15
 <212> PROTEIN
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 <400> 15
 EFSITDVVPYPISLR

<210> 16
 <211> 9
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 <213> UNKNOWN
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 <400> 16
 EIIDLVLDR

<210> 17
 <211> 15
 <212> PROTEIN
 <213> UNKNOWN
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 <400> 17
 AVFVDLEPTVIDEVR

<210> 18
 <211> 18
 <212> PROTEIN
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 VGINYQPPTVVPGGDLAK

<210> 19
 <211> 20
 <212> PROTEIN
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 <400> 19
 TIGGGDDSFNTFFSETGAGK

<210> 20
 <211> 13
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 <400> 20
 EIADGLCLEVEGK

<210> 21
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 <223> Fig. 4A - Spot 9 - Chaperonin groEL precursor
 <400> 21

TLNDELEIIEGMK

<210> 22

<211> 13

<212> PROTEIN

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<223> Fig. 4A - Spot 9 - Chaperonin groEL precursor

<400> 22

CEFQDAYVLLSEK

<210> 23

<211> 17

<212> PROTEIN

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<223> Fig. 4A - Spot 9 - Chaperonin groEL precursor

<400> 23

AAVEEGIVLGGGALLR

<210> 24

<211> 18

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 9 - Chaperonin groEL precursor

<400> 24

ISSVQSIVPALEIANHR

<210> 25

<211> 11

<212> PROTEIN

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<223> Fig. 4A - Spot 10 heat shock protein 74 kDa

<400> 25

VQQTVDLDFGR

<210> 26

<211> 14

<212> PROTEIN

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<223> Fig. 4A - Spot 10 heat shock protein 74 kDa

<400> 26

SDIGEVILVGGMTR

<210> 27

<211> 15

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 10 heat shock protein 74 kDa

<400> 27

LLGQFTLIGIPPAPR

<210> 28

<211> 15

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4A - Spot 10 heat shock protein 74 kDa

<400> 28

NAVITVPAYFNDSQR

<210> 29
<211> 15
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<400> 29
QVLLSAAEAAEVILR

<210> 30
<211> 16
<212> PROTEIN
<213> UNKNOWN
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<400> 30
EALLSSAVDHGSDEAR

<210> 31
<211> 18
<212> PROTEIN
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<223> Fig. 4A - Spot 12 Enolase 1, 2, or 3 (alpha, beta, or gamma)
<400> 31
AAVPSGASTGIYEALRL

<210> 32
<211> 14
<212> PROTEIN
<213> UNKNOWN
<223> Fig. 4A - Spot 13 - dnak-type molecular chaperone grp78 precursor
<400> 32
ITBSYVAFTPEGER

<210> 33
<211> 17
<212> PROTEIN
<213> UNKNOWN
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<400> 33
VTHAVVTVPAYFNDAQR

<210> 34
<211> 18
<212> PROTEIN
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<400> 34
DNHLLGTFDLTGIPPAPR

<210> 35
<211> 13
<212> PROTEIN
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<400> 35
FAAATGATPIAGR

<210> 36
<211> 10
<212> PROTEIN
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<400> 36
YVDIAIPCNNK

<210> 37
<211> 15
<212> PROTEIN
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<400> 37
FTPGTFTNQIQAAFR

<210> 38
<211> 17
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<223> Fig. 4A - Spot 14 Lamin receptor 1; p40-3, functional; p40-8, functional
<400> 38
AIVAIENPADVSVISSR

<210> 39
<211> 9
<212> PROTEIN
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<400> 39
YLTVAAVFR

<210> 40
<211> 9
<212> PROTEIN
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<400> 40
PGQLNADLR

<210> 41
<211> 10
<212> PROTEIN
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ISEQFTAMFR

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<212> PROTEIN
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ISEQFTAMFR

<210> 43

<211> 9
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AVFPSIVGR

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AVFPSIVGR

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SYELPDGQVITIGNER

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PVLLTEAPLNPK

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DAGTIA

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VVTV

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AAVPSGASTGIYEALRL

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GNPTVEVDLYTAK

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YITPDQLADLYK

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<211> 18
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AAVPSGASTGIYEALRL

<210> 63
<211> 9
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ETIA

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EFSITDVV

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<400> 67
VLATAFD

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ETIA

<210> 69
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TTLNA

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<223> Fig. 4B - Spot 7 - novel method

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YQPPTVV

<210> 73

<211> 14

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4B - Spot 7 - novel method

<400> 73

DSFNTFFSETGAGK

<210> 74

<211> 9

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4B - Spot 7 - Colloidal Coomassie

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EIIDLVLDLDR

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<211> 15

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4B - Spot 7 - Colloidal Coomassie

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AVFVDLEPTVIDEVR

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<211> 8

<212> PROTEIN

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<223> Fig. 4B - Spot 7 - Colloidal Coomassie

<400> 76

YQPPTVVP

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<211> 14

<212> PROTEIN

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<223> Fig. 4B - Spot 7 - Colloidal Coomassie

<400> 77

DSFNTFFSETGAGK

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<223> Fig. 4B - Spot 8 - novel method

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<210> 79

<211> 13

<212> PROTEIN

<213> UNKNOWN

<223> Fig. 4B - Spot 8 - Colloidal Coomassie

<400> 79

EIADGLCLEVEGK

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<211> 13

<212> PROTEIN

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<223> Fig. 4B - Spot 9 - novel method

<400> 80

TLNDELEIIEGMK

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<223> Fig. 4B - Spot 9 - novel method

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<210> 82

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EEGIVLOOCALLR

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QSIVPALEIA

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CEFQDAYVLLSEK

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SIVPALEIA

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FTLI

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VVTVPAYF

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TGIP

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FAAATGAT

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YVDIAIPCNNK

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FAAATGAT

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SYELPDGQVITIGNER

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PVLLTEAPLNPK

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VVTV

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DAGTIAGLNVLR

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VVTV

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PGVLIQVY

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YITP

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GNPTVEVDLY

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YITPDQLADLYK

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AAVPSGASTGIYEALRL

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TDVV

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EIIDLVLDLDR

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AVFVDLEPTVIDEVR

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EIIDLVLDR

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VDLEPTVI

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EGIVLGG

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